

We claim:

1. An array of genes each comprising an E-box regulatory sequence in its promoter, interacting with a gene binding to the E-box regulatory sequence or whose expression is dependent on this binding.
2. The array of claim 1 wherein the genes further comprise sequences encoding proteins associated with a particular state, disease or disorder.
3. The array of claim 2 wherein the state is age.
4. The array of claim 3 wherein the genes are isolated from a young animal.
5. The array of claim 3 wherein the genes are isolated from an old animal.
6. The array of claim 2 further comprising housekeeping genes whose expression does not change significantly as the state changes.
7. The array of claim 6 comprising at least nine housekeeping genes.
8. The array of claim 6 wherein the state is age and the expression of the housekeeping genes does not change as the animals age.
9. The array of claim 8 wherein the housekeeping genes are selected from the group consisting of tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, hypoxanthine phosphoribosyltransferase I (Lesh-Nyhan syndrome), Major histocompatibility complex, class I, C, Ubiquitin C, Glyceraldehyde-3-phosphate dehydrogenase, Human mRNA fragment encoding cytoplasmic actin, 60S Ribosomal protein L13A, and Aldolase C.
10. The array of claim 1 wherein the genes are present in nanomolar quantities.
11. A set of primers for use in detecting changes in expression of genes comprising an E-box regulatory sequence in its promoter or interacting with a gene binding to the E-box regulatory sequence, having a length between 480 and 700 base pairs length and a melting point between 75 and 85°C, wherein the primers include non-consensus sequence with protein coding sequence so that there is no detectable hybridization between homologous genes.
12. The set of primers of claim 11 where there is no hybridization between homologous genes.

13. The set of primers of claim 11 wherein the primers do not hybridize to homologous genes having the same degree of homology and c-myc and c-myc associated genes.
14. The set of primers of claim 11 comprising a label.
15. The set of primers of claim 14 wherein the label is selected from the group consisting of digoxigenine label, radiolabels and fluorescent labels.
16. A kit for detecting changes in expression of genes which is associated with a particular state, disease or disorder comprising
 - a) an array of genes each comprising an E-box regulatory sequence in its promoter or interacting with a gene binding to the E-box regulatory sequence and one or more housekeeping genes;
 - b) a set of E-box primers for use in detecting changes in expression of the genes in the array; and
 - c) means for detecting hybridization between the primers and the regulatory sequences.
17. The kit of claim 16 wherein the array of genes is prepared from cells or tissues of an animal characterized by a particular state, disease or disorder.
18. The kit of claim 17 wherein the animal is selected based on age or a disease or disorder associated with cancer, the neuronal system, the musculoskeletal system, or cardiovascular system.
19. The kit of claim 17 further comprising means for quantitating the amount of expression.
20. The kit of claim 18 wherein the animal or cells from which the genes are derived have been treated with one or more compounds or dosage regimes to screen for an effect of the compound or dosage regime on the state, disease or disorder.
21. A method of detecting changes in expression of genes associated with a particular state, disease or disorder comprising
 - a) providing an array of genes comprising an E-box regulatory sequence in its promoter or interacting with a gene binding to the E-box regulatory sequence;

b) providing a set of primers for use in detecting changes in expression of genes comprising an E-box regulatory sequence in its promoter or interacting with a gene binding to the E-box regulatory sequence, having a length between 480 and 700 base pairs length and a melting point between 75 and 85°C, wherein the primers include non-consensus sequence with protein coding sequence so that there is no detectable hybridization between homologous genes comprising a label;

c) providing the array of genes comprising an E-box regulatory sequence in its promoter or interacting with a gene binding to the E-box regulatory sequence and sequences encoding proteins associated with a particular state, disease or disorder further comprising housekeeping genes whose expression does not change significantly as the state, disease or disorder changes; and

d) reacting the primers with the genes.

22. A method for screening for differential expression of one or more E-box regulatory genes or genes interacting with genes binding to the E-box regulatory sequence, comprising:

- a) providing a first library associated with a particular disease, disorder or state,
- b) providing a second library of DNA obtained from cells having a different state or exposed to a compound to be tested,
- c) detecting or measuring expression of selected genes in the second library,
- d) comparing the expression of the selected genes in the first and second libraries, and
- e) detecting which genes have altered expression in the second DNA library.

23. The method of claim 22 wherein the state is selected from the group consisting of age, cancer and diseases or disorders of the cardiovascular, neurological, musculoskeletal, systems.

24. The method of claim 22 wherein the compound is a drug or toxin.

25. The method of claim 22 further comprising normalizing results of expression by comparison with housekeeping genes.
26. A method for determining the effect of a compound, disease or state of an individual comprising:
- a) providing a DNA library including one or more E-box regulatory genes or genes interacting with genes binding to the E-box regulatory sequence from the individual after treatment of the individual, cells or tissues derived therefrom with the compound or a particular dosage regime of the compound,
 - b) screening the library for changes in levels of expression of the selected genes, and
 - c) correlating the changes in expression with the state, disease or disorder prior to treatment.
27. The method of claim 26 wherein the cells or tissues are treated with one or more compounds *in vitro* prior to making the DNA library.
28. The method of claim 26 wherein the compound is selected from the group consisting of proteins or peptides, sugars or polysaccharides, nucleic acid molecules, and synthetic molecules.
29. The method of claim 26 wherein the library is derived from cells obtained from an individual of a particular age, having a particular disease or disorder, or derived from the neurological system, the cardiovascular system, the musculoskeletal system, or cancerous tissues.